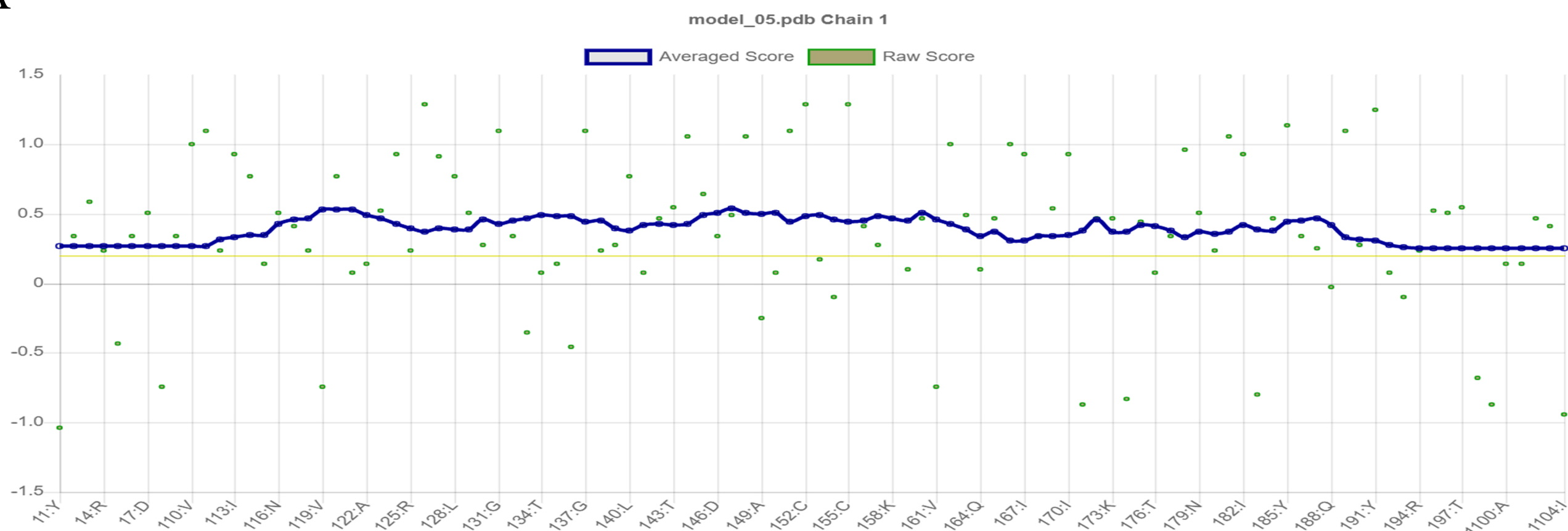
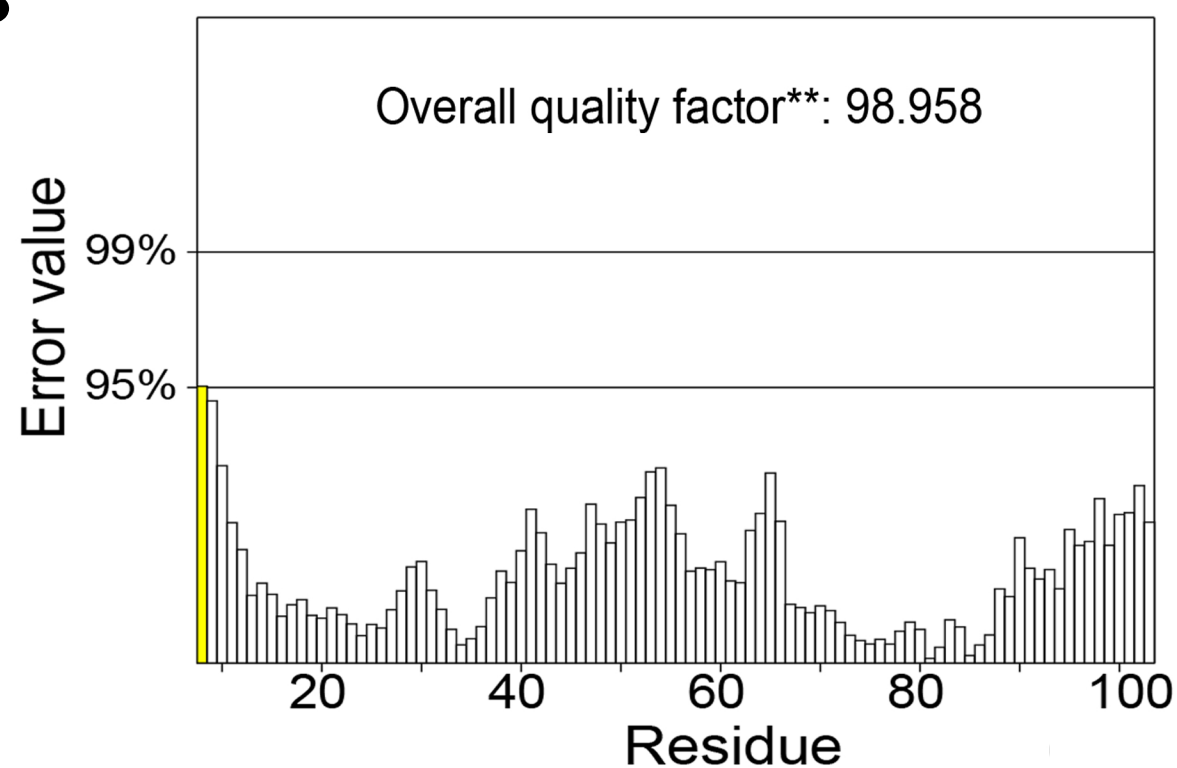


A



B



\*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

\*\*Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

C

Figure S1. Quality evaluation of the SnitCSP2 model. (A) Ramachandran plot; (B) Verify-3D; (C) ERRAT.